05/17



## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number:	10	1014	,099A			
Source:			OIPE			
Date Processed by STIC:	5	5/31	(or			
		1 .				

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002

## **Does Not Comply** Corrected Diskette Needed



OIPE

RAW SEQUENCE LISTING DATE: 05/31/2002 PATENT APPLICATION: US/10/014,099A TIME: 10:06:08

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\05312002\J014099A.raw

```
5 <110> APPLICANT: KUEHN, Ralf
             FELDER, Susanne
      7
             SCHWENK, Frieder
             KUETER LUKS, Birgit
      8
     9
             FAUST, Nicole
    11 <120> TITLE OF INVENTION: Modified Recombinase
    13 <130> FILE REFERENCE: 012787wo/JH/ml
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/014,099A
C--> 16 <141> CURRENT FILING DATE: 2001-12-11
     18 <160> NUMBER OF SEQ ID NOS: 108
```

## ERRORED SEQUENCES

change to 1408 <210> SEQ ID NO: 23 1409 <211> LENGTH: \_620

1410 <212> TYPE: (DNA )

1411 <213> ORGANISM: Artificial Sequence

20 <170> SOFTWARE: PatentIn Ver. 2.1

W--> 1412 <220> FEATURE: 1413 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA sequence

encoding the fusion protein C31-Int(CNLS) 1416 <400> SEQUENCE: 23 1417 Met Thr Gln Gly Val Val Thr Gly Val Asp Thr Tyr Ala Gly Ala Tyr

1418 1420 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala 1421 20 25

1423 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu 40

1426 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu

1429 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu

1432 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val

85 90 1435 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro

1436 100 105 1438 Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln

1439 115 120 125 1441 Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile

130 135 140

1444 Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys 1445 145 150 155 160

Input Set : A:\PTOMS.txt

1447 1448	Ile	Leu	Asp	Thr	Lys 165	Asn	Leu	Gln	Arg	Glu 170	Leu	Gly	Gly	Tyr	Val 175	Gly
1450	Glv	Lvs	Ala	Pro	Tvr	Glv	Phe	Glu	Leu		Ser	Glu	Thr	Tivs		Tle
1451	0-1	-1-		180	-1-	1			185					190	<b>0</b> _u	
1453	Thr	Δτα	Δen		Δra	Met	Val	Δan		Val	T1_	Δen	T.vc		λla	Uic
1454	7 111	пта	195	GIÃ	ary	MCC	Vul	200	Val	vai	116	VOII	205	шeu	MIG	птэ
1456	Con	mb =		Dro	T 011	mh ~	C1		Dho	C1.,	Dha	C1		7.00	3707	<del>-</del> 1-
	ser		TIIT	PIO	ьеu	TIII	215	PIO	rne	GIU	Pile		PIO	ASP	Val	TTE
1457	3	210	M	M	7	<b>a</b> 1		T	m1	TT 4 -	T	220	T	<b>D</b>	D1-	<b>.</b>
1459		ттр	Trp	ттр	Arg		TTE	ьys	Thr	HIS		HIS	Leu	Pro	Рпе	
1460		~ 3	_			230		1	_		235				_	240
1462	Pro	GTĀ	Ser	Gin		Ala	пте	His	Pro		Ser	lle	Thr	GLY		Cys
1463	_			_	245		_ •	<b>-</b>	_	250	_				255	
1465	Lys	Arg	Met	_	Ala	Asp	Ala	Val		Thr	Arg	GТĀ	Glu		Ile	Gly
1466				260					265					270		
1468	Lys	Lys		Ala	Ser	Ser	Ala		Asp	Pro	Ala	Thr	Val	Met	Arg	Ile
1469			275					280					285			
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1472		290					295					300				
1474	Lys	Lys	Pro	Asp	Gly	Thr	Pro	Thr	Thr	Lys	Ile	Glu	Gly	Tyr	Arg	Ile
1475						310					315					320
1477	Gln	Arg	Asp	Pro	Ile	Thr	Leu	Arg	Pro	Val	Glu	Leu	Asp	Cys	Gly	Pro
1478					325					330					335	
1480	Ile	Ile	Glu	Pro	Ala	Glu	$\mathtt{Trp}$	Tyr	Glu	Leu	Gln	Ala	Trp	Leu	Asp	Gly
1481				340					345					350		
1483	Arg	Gly	Arg	Gly	Lys	Gly	Leu	Ser	Arg	Gly	Gln	Ala	Ile	Leu	Ser	Ala
1484			355					360					365			
1486	Met	Asp	Lys	Leu	Tyr	Cys	Glu	Cys	Gly	Ala	Val	Met	Thr	Ser	Lys	Arg
1487		370					375					380				
1489	Gly	Glu	Glu	Ser	Ile	Lys	Asp	Ser	Tyr	Arg	Cys	Arg	Arg	Arg	Lys	Val
1490	385					390					395					400
1492	Val	Asp	Pro	Ser	Ala	Pro	Gly	Gln	His	Glu	Gly	Thr	Cys	Asn	Val	Ser
1493					405					410					415	
1495	Met	Ala	Ala	Leu	Asp	Lys	Phe	Val	Ala	Glu	Arg	Ile	Phe	Asn	Lys	Ile
1496				420					425					430		
1498	Arg	His	Ala	Glu	Gly	Asp	Glu	Glu	Thr	Leu	Ala	Leu	Leu	Trp	Glu	Ala
1499			435					440					445			
1501	Ala	Arg	Arg	Phe	Gly	Lys	Leu	Thr	Glu	Ala	Pro	Glu	Lys	Ser	Gly	Glu
1502		450					455					460				
1504	Arg	Ala	Asn	Leu	Val	Ala	Glu	Arg	Ala	Asp	Ala	Leu	Asn	Ala	Leu	Glu
1505						470					475					480
1507	Glu	Leu	Tyr	Glu	Asp	Arg	Ala	Ala	Gly	Ala	Tyr	Asp	Gly	Pro	Val	Gly
1508			_		485	-			_	490	-	_	_		495	-
1510	Arg	Lys	His	Phe	Arg	Lys	Gln	Gln	Ala	Ala	Leu	Thr	Leu	Arq	Gln	Gln
1511	_	_		500	~	-			505					510		
1513	Gly	Ala	Glu	Glu	Arg	Leu	Ala	Glu		Glu	Ala	Ala	Glu		Pro	Lys
1514	-		515		,			520					525			-
1516	Leu	Pro	Leu	Asp	Gln	Trp	Phe		Glu	Asp	Ala	Asp		Asp	Pro	Thr
1517		530		•		•	535			•		540		•		_
1519	Gly	Pro	Lys	Ser	Trp	Trp	Gly	Arg	Ala	Ser	Val	Asp	qaA	Lys	Arq	Val
	-		-		•	-	-									_

Input Set : A:\PTOMS.txt

```
550
    1520 545
    1522 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
                                         570
                      565
    1525 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
    1526 580
                                      585
    1528 Ala Lys Pro Pro Thr Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
                                 600
    1531 Glu Asp Val Ala Ala Pro Lys Lys Arg Lys Val
E--> 1532 610
                               615
    3321 <210> SEQ ID NO: 65
    3322 <211> LENGTH: 335
    3323 <212> TYPE: PRT
                                                      12207 is mandatury and needs to be inserted
    3324 <213> ORGANISM: Artificial Sequence
W--> 3325 (220) FEATURE
    3325 <223> OTHER INFORMATION: Description of Artificial Sequence: vector
    3326 pBS-SSV3
E--> 3328 <400> SEQUENCE: 65
    3329 Met Thr Lys Asp Lys Thr Arg Tyr Lys Tyr Gly Asp Tyr Ile Leu Arg
    3332 Glu Arg Lys Gly Arg Tyr Tyr Val Tyr Lys Leu Glu Tyr Glu Asn Gly
                                       25
          20
    3335 Glu Val Lys Glu Arg Tyr Val Gly Pro Leu Ala Asp Val Val Glu Ser
                                   40
    3338 Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala
    3341 Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Lys
    3342 65
                                              75
                           70
    3344 Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln
                        8.5
                                          90
    3347 Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn
    3350 Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile
    3351 115
                                   120
    3353 Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu
                               135
    3356 Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala
    3357 145
                           150
                                              155
    3359 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Lys Ala Asn Ala Asp Ile
                                          170
                       165
    3362 Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys
                   180
                                      185
    3365 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser
                                   200
    3368 Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg
                               215
    3371 Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg
    3372 225 230
                                             235
    3374 Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg
                        245
                                          250
```

Input Set : A:\PTOMS.txt

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3377 Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys
                  260
                                    265
    3380 Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met
    3381 275
                                280
                                                   285
    3383 Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg
                             295
    3386 Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile
                                            315
    3387 305
                         310
    3389 Ala Lys Glu Gln Tyr Lys Lys Tyr Ala Glu Trp Leu Lys Gly Val
                      325
                              330
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    3530 <211> LENGTH: 479
    3531 <212> TYPE: PRT
3533 <del>223></del> OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
    3534 coding for fusion protein NLS-XisA
E--> 3536 <400> SEQUENCE: 67
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                                         10
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          20
                                      25
    3543 Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Arg Glu His Met Arg
    3544 35
                                  40
    3546 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser
    3547 50
                              55
    3549 Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu
                          70
                                             75
    3552 Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr
                       85
                                         90
    3555 Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp
                                     105
                   100
    3558 Gly Leu Lys Thr Ala Glu Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile
                                 120
    3559 115
    3561 Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala
                              135
    3564 Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala
                                            155
                          150
    3567 Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr
                     165
                                        170
    3570 Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp
                  180
                                 185
    3573 Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys
         195
                                 200
    3576 Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile
          210
                             215
                                               220
    3579 Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp
    3580 225 230
                                            235
    3582 Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile
```

Input Set : A:\PTOMS.txt

```
245
                                        250
    3585 Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu
    3586 260
                                    265
    3588 Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu
    3589 275
                                280
    3591 Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile
    3592 290 295
    3594 Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp
                         310
    3597 Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu
                     325
                            330 335
    3600 Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu
                                   345
    3603 Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr
                                360
    3606 Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp
    3607 370 375
    3609 Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile
                         390
                                           395
    3612 Leu Gly Ile Pro Ile Lys Ala Ala Asp Asn Leu Gly His Ser Met
         405
                                     410
    3615 Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg
    3616 420
                                  425 430
    3618 Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val
    3619 435
                                440
    3621 Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg
    3622 450 455
    3624 Met Glu Ile Glu Lys Leu Lys Met Glu Ile Ala Tyr Lys Asn Ser
    3732 <210> SEQ ID NO: 69
    3733 <211> LENGTH: 342
3735 <213> ORGANISM: Artificial Sequence (2207 is mandalon and w--> 3736 <2207 FEATURE:
    3736 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
    3737 coding for fusion protein NLS-Ssv
E--> 3739 <400> SEQUENCE: 69
    3740 Met Pro Lys Lys Lys Arg Lys Val Thr Lys Asp Lys Thr Arg Tyr Lys
    3743 Tyr Gly Asp Tyr Ile Leu Arg Glu Arg Lys Gly Arg Tyr Tyr Val Tyr
    3744 20
                                    25
    3746 Lys Leu Glu Tyr Glu Asn Gly Glu Val Lys Glu Arg Tyr Val Gly Pro
    3749 Leu Ala Asp Val Val Glu Ser Tyr Leu Lys Met Lys Leu Gly Val Val
                              55
    3752 Gly Asp Thr Pro Leu Gln Ala Asp Pro Pro Gly Phe Glu Pro Gly Thr
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    3755 Ser Gly Ser Gly Gly Gly Lys Glu Gly Thr Glu Arg Arg Lys Ile Ala
    3756
                       85
                                         90
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Input Set : A:\PTOMS.txt

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3761	Phe	Tyr	Asn	$\mathtt{Tyr}$	Leu	Met	Asn		Arg	Gly	Ile	Ser	Glu	Lys	Thr	Ala
3762			115	_				120					125			
3764	Lys		Tyr	Ile	Asn	Ala		Ser	Lys	Pro	Tyr		Glu	Thr	Arg	Asp
3765		130				•	135	<b>51</b>		•	<b>51.</b> -	140	- 1 -	<b>a</b>	•	
3767		GIn	гàг	Ата	Tyr	Arg 150	Leu	Pne	Ата	Arg		ьеи	Ата	ser	Arg	
3768 3770		т1 ^	uic	) an	Clu		λ1 5	λαn	Tvc	т1 о	155	Tvc	λla	Wa 1	Tare	160
3771	116	116	птэ	изр	165	FIIE	мта	изр	БУЗ	170	neu	цуз	ніа	Val	175	Val
3773	Lvs	Lvs	Ala	Asn		Asp	Tle	Tvr	Tle		Thr	Len	Glu	Glu		Lvs
3774	-1-	-1-		180				-1-	185					190		-1-
3776	Arg	Thr	Leu	Gln	Leu	Ala	Lys	Asp	Tyr	Ser	Glu	Asn	Val	Tyr	Phe	Ile
3777	_		195				-	200	-				205	-		
3779	Tyr	Arg	Ile	Ala	Leu	$\operatorname{Glu}$	Ser	Gly	Val	Arg	Leu	Ser	Glu	Ile	Leu	Lys
3780		210					215					220				
3782		Leu	Lys	Glu	Pro	Glu	Arg	Asp	Ile	Cys	Gly	Asn	Asp	Val	Cys	Tyr
3783						230					235					240
3785	Tyr	Pro	Leu	Ser	-	Thr	Arg	Gly	$\mathtt{Tyr}$	_	Gly	Val	Phe	Tyr		Phe
3786		~ 1	<b>-1</b> .		245			1	<b>a1</b>	250	ml	<b>-</b>			255	
3788 3789	His	тте	Thr	260	Leu	гĀЗ	Arg	vaı	265	vai	Tur	гля	Trp		тте	ATa
3791	7 an	Dho	Clu		7 ~~	uic	Tvc	Nan		T10	7 l s	Tla	Lvo	270	Dho	λνα
3792	Asp	Pile	275	AIG	AIG	urs	пуъ	280	АІа	TTE	ніа	TTE	285	тАт	Pite	AIG
3794	T.v.s	Phe		Δla	Ser	T.vs	Met		Glu	T.e.ii	Ser	Va1		Len	Asn	Tle
3795	270	290	,		501	275	295		<b>u_u</b>	Dou	501	300		200	TIDP	110
3797	Ile		Phe	Ile	Gln	Gly		Lys	Pro	Thr	Arg		Leu	Thr	Gln	His
3798		-				310		*			315					320
3800	Tyr	Val	Ser	Leu	Phe	Gly	Ile	Ala	Lys	Glu	Gln	Tyr	Lys	Lys	Tyr	Ala
3801					325					330					335	
3803	Glu	$\mathtt{Trp}$	Leu		Gly	Val										
3804				340												
6191						3										
6192					35											
6193					Dood			1717	2001	- 1						
6194 6196						rerro	opnag	ge Ti	,90T.	_ T						
6197						λla	Tla	Патъ	Thr	Δτα	Va 1	Sor	Thr	Thr	λen	Gin
6198	1	1 111	пуз	пуз	5	пια	TIC	тут	1111	10	Val	Der	1111	1111	15	GIII
6200		Glu	Glu	Glv	_	Ser	Ile	Asp	Glu		Ile	Asp	Arσ	Leu		Lvs
6201																-1-
6203	Tyr	Ala	Glu	Ala	Met	Gly	Trp	Gln	Val	Ser	Asp	Thr	Tyr	Thr	Asp	Ala
6204	_		35			_	_	40			_		45		_	
6206	Gly	Phe	Ser	Gly	Ala	Lys	Leu	Glu	Arg	Pro	Ala	Met	Gln	Arg	Leu	Ile
6207		50					55					60				
6209		Asp	Ile	Glu	Asn	_	Ala	Phe	Asp	Thr		Leu	Val	$\mathtt{Tyr}$	Lys	
6210	65		_	_	_	70		_	_		75		_		_	80
6212	Asp	Arg	Leu	Ser		Ser	Val	Arg	Asp		Leu	Tyr	Leu	Val	_	Asp
6213					85					90					95	



Input Set : A:\PTOMS.txt

6215	Val	Phe		Lys 100	Asn	Lys	Ile	Asp	Phe 105	Ile	Ser	Leu	Asn	Glu 110	Ser	Ile
6216 6218	3	mh-x	Cor	Sor	Δla	Met	Glv			Phe	Leu	Thr	Ile	Leu	Ser	Ala
	ASP	THI	115	261	лта	Mee	O-1	120					125			
6219 6221	т1.	λαη	Glu	Dhe	Glu	Ara	Glu	Asn	Ile	Lys	Glu	Arg	Met	Thr	Met	Gly
C222		120					135					140				
6222 6224	T G	130	C117	λτα	Δla	Lvs	Ser	Glv	Lvs	Ser	Met	Met	Trp	Thr	Lys	Thr
C00F	1 4 5					150					TOO					100
6225 6227	143	Dho	C1v	ጥኒፖ	Tur	His	Asn	Ara	Lvs	Thr	Gly	Ile	Leu	Glu	Ile	Val
	Ald	Pile	GIY	ıyı	165	1115	11011	5	-1-	170	•				175	
6228 6230	Dro	LOU	Gln.	Δla	Thr	Tle	Val	Glu	Gln	Ile	Phe	Thr	Asp	Tyr	Leu	Ser
C 2 2 1				180					185					130		
6231 6233	C1v	т1Д	Ser	Leu	Thr	Lvs	Leu	Arq	Asp	Lys	Leu	Asn	$\operatorname{Glu}$	Ser	Gly	His
6721			195					200					203			
6236	т1Б	Glv	Lvs	Asp	Ile	Pro	Trp	Ser	Tyr	Arg	Thr	Leu	Arg	Gln	Thr	Leu
6027		210					215					220				
6237	Δsn	Asn	Pro	Val	Tyr	Cys	Gly	Tyr	Ile	Lys	Phe	Lys	Asp	Ser	Leu	Phe
C 0 4 0	225					230					233					210
6242	Glu	Glv	Met	His	Lys	Pro	Ile	Ile	Pro	Tyr	Glu	Thr	Tyr	Leu	Lys	Val
(242					245					∠⊃v					233	
6245	Gln	Lvs	Glu	Leu	Glu	Glu	Arg	Gln	Gln	Gln	Thr	$\mathtt{Tyr}$	Glu	Arg	Asn	Asn
C046				260					265					2/0		
6248	Asn	Pro	Arg	Pro	Phe	Gln	Ala	Lys	Tyr	Met	Leu	Ser	Gly	Met	Ala	Arg
(240			275					280					203			
6251	Cys	Gly	Tyr	Cys	Gly	Ala	Pro	Leu	Lys	Ile	Val	Leu	Gly	His	Lys	Arg
COFO		200					295					300				
6252 6254	Lys	Asp	Gly	Ser	Arg	Thr	Met	Lys	Tyr	His	Cys	Ala	Asn	Arg	Pne	220
6255	205					310					213					320
6257	Arg	Lys	Thr	Lys	Gly	Ile	Thr	Val	$\mathtt{Tyr}$	Asn	Asp	Asn	гаг	гуз	CYS	ASP
6258					325				_	330	• • • • • •	m la an	17.01	T10	335	
6260	Ser	Gly	Thr	Tyr	Asp	Leu	Ser	Asn	Leu	GIU	ı Asn	Thr	vaı	350	. Ash	Asn
6261				340		_	_	_	345			Tou	T 170			λen
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/014,099A

DATE: 05/31/2002 TIME: 10:06:09

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\05312002\J014099A.raw

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6288

485

file://C:\Crf3\Outhold\VsrJ014099A.htm



VERIFICATION SUMMARY
PATENT APPLICATION: US/10/014,099A

TIME: 05/31/2002
TIME: 10:06:10

Input Set : A:\PTOMS.txt

Output Set: N:\CRF3\05312002\J014099A.raw

L:15 M:270 C: Current Application Number differs, Replaced Application Number L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:262 M:256 W: Invalid Numeric Header Field, <220> has non-blank data L:263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10 L:921 M:256 W: Invalid Numeric Header Field, <220> has non-blank data L:922 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19 L:928 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19 L:937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:480 L:1412 M:283 W: Missing Blank Line separator, <220> field identifier L:1532 M:252 E: No. of Seq. differs, <211> LENGTH:Input:620 Found:0 SEQ:23 L:3325 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:65 L:3328 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:65 L:3533 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67 L:3536 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:67 L:3736 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:69 L:3739 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:69 L:6294 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:108